



#7

SEQUENCE LISTING

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The Government of the United States of America
as represented by The Secretary of the
Department of Health and Human Services

<120> Methods of Diagnosing Multidrug Resistant Tuberculosis

<130> 015280-413100US

<140> US 09/888,320

<141> 2001-06-22

<150> US 60/214,187

<151> 2000-06-26

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 1867

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> wild-type EtaA monooxygenase (Rv3854c, EthA)

<220>

<221> CDS

<222> (201)..(1670)

<223> EtaA

<400> 1

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ccggacggcc gcgcggtgcg ccggccccta ggcagcgaag cctgactggc cgcgagggtg 120

gtcaccctgg cagcttacta cgtgtcgata gtgtcgacat ctggttgacg gcctcgacat 180

tacgttgata gcgtggatcc atg acc gag cac ctc gac gtt gtc atc gtg ggc 233

Met Thr Glu His Leu Asp Val Val Ile Val Gly

1

5

10

gct gga atc tcc ggt gtc agc gcg gcc tgg cac ctg cag gac cgt tgc 281

Ala Gly Ile Ser Gly Val Ser Ala Ala Trp His Leu Gln Asp Arg Cys

15

20

25

ccg acc aag agc tac gcc atc ctg gaa aag cgg gaa tcc atg ggc ggc 329

Pro Thr Lys Ser Tyr Ala Ile Leu Glu Lys Arg Glu Ser Met Gly Gly

30

35

40

acc tgg gat ttg ttc cgt tat ccc gga att cgc tcc gac tcc gac atg 377

Thr Trp Asp Leu Phe Arg Tyr Pro Gly Ile Arg Ser Asp Ser Asp Met

45

50

55

tac acg cta ggt ttc cga ttc cgt ccc tgg acc gga cgg cag gcg atc	425
Tyr Thr Leu Gly Phe Arg Phe Arg Pro Trp Thr Gly Arg Gln Ala Ile	
60 65 70 75	
gcc gac ggc aag ccc atc ctc gag tac gtc aag agc acc gcg gcc atg	473
Ala Asp Gly Lys Pro Ile Leu Glu Tyr Val Lys Ser Thr Ala Ala Met	
80 85 90	
tat gga atc gac agg cat atc cgg ttc cac cac aag gtg atc agt gcc	521
Tyr Gly Ile Asp Arg His Ile Arg Phe His His Lys Val Ile Ser Ala	
95 100 105	
gat tgg tcg acc gcg gaa aac cgc tgg acc gtt cac atc caa agc cac	569
Asp Trp Ser Thr Ala Glu Asn Arg Trp Thr Val His Ile Gln Ser His	
110 115 120	
ggc acg ctc agc gcc ctc acc tgc gaa ttc ctc ttt ctg tgc agc gcc	617
Gly Thr Leu Ser Ala Leu Thr Cys Glu Phe Leu Phe Leu Cys Ser Gly	
125 130 135	
tac tac aac tac gac gag ggc tac tcg ccg aga ttc gcc gcc tcg gag	665
Tyr Tyr Asn Tyr Asp Glu Gly Tyr Ser Pro Arg Phe Ala Gly Ser Glu	
140 145 150 155	
gat ttc gtc ggg ccg atc atc cat ccg cag cac tgg ccc gag gac ctc	713
Asp Phe Val Gly Pro Ile Ile His Pro Gln His Trp Pro Glu Asp Leu	
160 165 170	
gac tac gac gct aag aac atc gtc gtg atc ggc agt ggc gca acg gcg	761
Asp Tyr Asp Ala Lys Asn Ile Val Val Ile Gly Ser Gly Ala Thr Ala	
175 180 185	
gtc acg ctc gtg ccg gcg ctg gcg gac tcg ggc gcc aag cac gtc acg	809
Val Thr Leu Val Pro Ala Leu Ala Asp Ser Gly Ala Lys His Val Thr	
190 195 200	
atg ctg cag cgc tca ccc acc tac atc gtg tcg cag cca gac cgg gac	857
Met Leu Gln Arg Ser Pro Thr Tyr Ile Val Ser Gln Pro Asp Arg Asp	
205 210 215	
ggc atc gcc gag aag ctc aac cgc tgg ctg ccg gag acc atg gcc tac	905
Gly Ile Ala Glu Lys Leu Asn Arg Trp Leu Pro Glu Thr Met Ala Tyr	
220 225 230 235	
acc gcg gta cgg tgg aag aac gtg ctg cgc cag gcg gcc gtg tac agc	953
Thr Ala Val Arg Trp Lys Asn Val Leu Arg Gln Ala Ala Val Tyr Ser	
240 245 250	
gcc tgc cag aag tgg cca cgg cgc atg cgg aag atg ttc ctg agc ctg	1001
Ala Cys Gln Lys Trp Pro Arg Arg Met Arg Lys Met Phe Leu Ser Leu	
255 260 265	
atc cag cgc cag cta ccc gag ggg tac gac gtg cga aag cac ttc gcc	1049
Ile Gln Arg Gln Leu Pro Glu Gly Tyr Asp Val Arg Lys His Phe Gly	
270 275 280	
ccg cac tac aac ccc tgg gac cag cga ttg tgc ttg gtg ccc aac gcc	1097
Pro His Tyr Asn Pro Trp Asp Gln Arg Leu Cys Leu Val Pro Asn Gly	
285 290 295	

gac ctg ttc cgg gcc att cgt cac ggg aag gtc gag gtg gtg acc gac Asp Leu Phe Arg Ala Ile Arg His Gly Lys Val Glu Val Val Thr Asp 300 305 310 315	1145
acc att gaa cgg ttc acc gcg acc gga atc cgg ctg aac tca ggt cgc Thr Ile Glu Arg Phe Thr Ala Thr Gly Ile Arg Leu Asn Ser Gly Arg 320 325 330	1193
gaa ctg ccg gct gac atc atc att acc gca acg ggg ttg aac ctg cag Glu Leu Pro Ala Asp Ile Ile Ile Thr Ala Thr Gly Leu Asn Leu Gln 335 340 345	1241
ctt ttt ggt ggg gcg acg gcg act atc gac gga caa caa gtg gac atc Leu Phe Gly Gly Ala Thr Ala Thr Ile Asp Gly Gln Gln Val Asp Ile 350 355 360	1289
acc acg acg atg gcc tac aag ggc atg atg ctt tcc ggc atc ccc aac Thr Thr Thr Met Ala Tyr Lys Gly Met Met Leu Ser Gly Ile Pro Asn 365 370 375	1337
atg gcc tac acg gtt ggc tac acc aat gcc tcc tgg acg ctg aag gcc Met Ala Tyr Thr Val Gly Tyr Thr Asn Ala Ser Trp Thr Leu Lys Ala 380 385 390 395	1385
gac ctg gtg tcg gag ttt gtc tgt cgc ttg ttg aat tac atg gac gac Asp Leu Val Ser Glu Phe Val Cys Arg Leu Leu Asn Tyr Met Asp Asp 400 405 410	1433
aac ggt ttt gac acc gtg gtc gtc gag cga ccg ggc tca gat gtc gaa Asn Gly Phe Asp Thr Val Val Val Glu Arg Pro Gly Ser Asp Val Glu 415 420 425	1481
gag cgg ccc ttc atg gag ttc acc cca ggt tac gtg ctg cgc tcg ctg Glu Arg Pro Phe Met Glu Phe Thr Pro Gly Tyr Val Leu Arg Ser Leu 430 435 440	1529
gac gag ctg ccc aag cag ggt tcg cgt aca ccg tgg cgc ctg aat cag Asp Glu Leu Pro Lys Gln Gly Ser Arg Thr Pro Trp Arg Leu Asn Gln 445 450 455	1577
aac tac cta cgt gac atc cgg ctc atc cgg cgc ggc aag atc gac gac Asn Tyr Leu Arg Asp Ile Arg Leu Ile Arg Arg Gly Lys Ile Asp Asp 460 465 470 475	1625
gag ggt ctg cgg ttc gcc aaa agg cct gcc ccg gtg ggg gtt tag Glu Gly Leu Arg Phe Ala Lys Arg Pro Ala Pro Val Gly Val 480 485 490	1670
ctttagcgac ggttttagcgc cggtttaggc catagtcaga cgacgatgat gccgtcgtcg	1730
tcgctgtagg cgatatcgcc cggaacgaat gtcaccccgcc ccagcgtgat ttcaacgtcg	1790
cgttctccgg caccggtctt ggtgctcttg cggggattgg tgcccagcgc tttgatgccg	1850
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<210> 2
 <211> 489
 <212> PRT
 <213> Mycobacterium tuberculosis
 <223> wild-type EtaA monooxygenase (Rv3854c, EthA)

<400> 2
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 Val Ser Ala Ala Trp His Leu Gln Asp Arg Cys Pro Thr Lys Ser Tyr
 20 25 30
 Ala Ile Leu Glu Lys Arg Glu Ser Met Gly Gly Thr Trp Asp Leu Phe
 35 40 45
 Arg Tyr Pro Gly Ile Arg Ser Asp Ser Asp Met Tyr Thr Leu Gly Phe
 50 55 60
 Arg Phe Arg Pro Trp Thr Gly Arg Gln Ala Ile Ala Asp Gly Lys Pro
 65 70 75 80
 Ile Leu Glu Tyr Val Lys Ser Thr Ala Ala Met Tyr Gly Ile Asp Arg
 85 90 95
 His Ile Arg Phe His His Lys Val Ile Ser Ala Asp Trp Ser Thr Ala
 100 105 110
 Glu Asn Arg Trp Thr Val His Ile Gln Ser His Gly Thr Leu Ser Ala
 115 120 125
 Leu Thr Cys Glu Phe Leu Phe Leu Cys Ser Gly Tyr Tyr Asn Tyr Asp
 130 135 140
 Glu Gly Tyr Ser Pro Arg Phe Ala Gly Ser Glu Asp Phe Val Gly Pro
 145 150 155 160
 Ile Ile His Pro Gln His Trp Pro Glu Asp Leu Asp Tyr Asp Ala Lys
 165 170 175
 Asn Ile Val Val Ile Gly Ser Gly Ala Thr Ala Val Thr Leu Val Pro
 180 185 190
 Ala Leu Ala Asp Ser Gly Ala Lys His Val Thr Met Leu Gln Arg Ser
 195 200 205
 Pro Thr Tyr Ile Val Ser Gln Pro Asp Arg Asp Gly Ile Ala Glu Lys
 210 215 220
 Leu Asn Arg Trp Leu Pro Glu Thr Met Ala Tyr Thr Ala Val Arg Trp
 225 230 235 240
 Lys Asn Val Leu Arg Gln Ala Ala Val Tyr Ser Ala Cys Gln Lys Trp
 245 250 255
 Pro Arg Arg Met Arg Lys Met Phe Leu Ser Leu Ile Gln Arg Gln Leu
 260 265 270
 Pro Glu Gly Tyr Asp Val Arg Lys His Phe Gly Pro His Tyr Asn Pro
 275 280 285
 Trp Asp Gln Arg Leu Cys Leu Val Pro Asn Gly Asp Leu Phe Arg Ala
 290 295 300
 Ile Arg His Gly Lys Val Glu Val Val Thr Asp Thr Ile Glu Arg Phe
 305 310 315 320
 Thr Ala Thr Gly Ile Arg Leu Asn Ser Gly Arg Glu Leu Pro Ala Asp
 325 330 335
 Ile Ile Ile Thr Ala Thr Gly Leu Asn Leu Gln Leu Phe Gly Gly Ala
 340 345 350
 Thr Ala Thr Ile Asp Gly Gln Gln Val Asp Ile Thr Thr Met Ala
 355 360 365
 Tyr Lys Gly Met Met Leu Ser Gly Ile Pro Asn Met Ala Tyr Thr Val
 370 375 380
 Gly Tyr Thr Asn Ala Ser Trp Thr Leu Lys Ala Asp Leu Val Ser Glu
 385 390 395 400
 Phe Val Cys Arg Leu Leu Asn Tyr Met Asp Asp Asn Gly Phe Asp Thr
 405 410 415
 Val Val Val Glu Arg Pro Gly Ser Asp Val Glu Glu Arg Pro Phe Met
 420 425 430

Glu Phe Thr .Pro Gly Tyr Val Leu Arg Ser Leu Asp Glu Leu Pro Lys
 435 440 445
 Gln Gly Ser Arg Thr Pro Trp Arg Leu Asn Gln Asn Tyr Leu Arg Asp
 450 455 460
 Ile Arg Leu Ile Arg Arg Gly Lys Ile Asp Asp Glu Gly Leu Arg Phe
 465 470 475 480
 Ala Lys Arg Pro Ala Pro Val Gly Val
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<210> 3
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:EtaA PCR
 amplification primer

<400> 3
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<210> 4
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:EtaA PCR
 amplification primer

<400> 4
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<210> 5
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:EtaA Primer 3
 sequencing primer, EtaA amplification primer

<400> 5
 atcatccatc cgcagcac

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<210> 6
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:EtaA Primer 3
 sequencing primer, EtaA amplification primer

<400> 6
 aagctgcagg ttcaacc

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<210> 7
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

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sequencing primer, EtaA amplification primer

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<210> 8
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<213> Artificial Sequence

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sequencing primer, EtaA amplification primer

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aagctgcagg ttcaacc

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<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EtaA Primer 3
sequencing primer, EtaA amplification primer

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tgaactcagg tcgccaac

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<210> 10
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:EtaA Primer 3
sequencing primer, EtaA amplification primer

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<210> 11
<211> 17
<212> DNA
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sequencing primer, EtaA amplification primer

<400> 11
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<210> 12
<211> 17
<212> DNA
<213> Artificial Sequence

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sequencing primer, EtaA amplification primer

<400> 12
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17

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

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sequencing primer, EtaA amplification primer

<400> 13
tctatttccc atccaag

17

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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sequencing primer, EtaA amplification primer

<400> 14
gccatgtcgg cttgattg

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<210> 15
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:EtaR PCR
amplification primer

<400> 15
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32

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:EtaR PCR
amplification primer

<400> 16

ataagaatgc ggccgcgcgg ttctcgccgt aaatgct

37